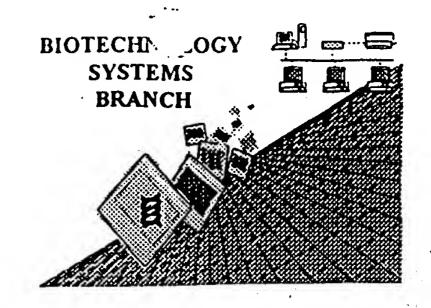# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/810, 861 A_

Source: _OIPE_

Date Processed by STIC: _7/5/2001_ BEST AVAILABLE COPY

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING　　　　　　　DATE: 07/05/2001
PATENT APPLICATION: US/09/810,861A　　TIME: 10:31:39

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\07052001\I810861A.raw**

Does Not Comply
Corrected Diskette Needed

see page 5

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   4        Hermona, Soreq
   5        Charles, Arntzen
   6        Hugh, Mason
   8 <120> TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
TRANSGENIC
   9        TOMATOES
  11 <130> FILE REFERENCE: BTI-45
  13 <140> CURRENT APPLICATION NUMBER: 09/810,861A
C-->  14 <141> CURRENT FILING DATE: 2001-06-18
  16 <150> PRIOR APPLICATION NUMBER: 06/190,440
  17 <151> PRIOR FILING DATE: 2000-03-17
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  35 <213> ORGANISM: Homo sapiens
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RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/810,861A   TIME: 10:31:39

Input Set : A:\PTO.txt
Output Set: N:\CRF3\07052001\I810861A.raw

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RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/810,861A   TIME: 10:31:39

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\07052001\I810861A.raw**

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RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/810,861A   TIME: 10:31:39

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RAW SEQUENCE LISTING　　　　　　　DATE: 07/05/2001
PATENT APPLICATION:　US/09/810,861A　　TIME: 10:31:39

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Output Set: N:\CRF3\07052001\I810861A.raw

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398 gtcattatag cgattttttc ggtatatcca tcctttttcg cacgatatac aggattttgc 4380
400 caaagggttc gtgtagactt ccttggtgt atccaacggc gtcagccggg caggataggt 4440
402 gaagtaggcc cacccgcgag cgggtgttcc ttcttcactg tcccttattc gcacctggcg 4500
404 gtgctcaacg ggaatcctgc tctgcgaggc tggccggcta ccgccggcgt aacagatgag 4560
406 ggcaagcgga tggctgatga aaccaagcca accaggaagg gcagcccacc tatcaaggtg 4620
408 tactgccttc cagacgaacg aagagcgatt gaggaaaagg cggcggcggc cggcatgagc 4680
410 ctgtcggcct acctgctggc cgtcggccag ggctacaaaa tcacgggcgt cgtggactat 4740
412 gagcacgtcc gcgagctggc ccgcatcaat ggcgacctgg ccgcctggg cggcctgctg 4800
414 aaactctggc tcaccgacga cccgcgcacg cgcgcggttcg gtgatgccac gatcctcgcc 4860
416 ctgctggcga agatcgaaga gaagcaggac gagcttggca aggtcatgat gggcgtggtc 4920
418 cgcccgaggg cagagccatg actttttag ccgctaaaac ggccgggggg tgcgcgtgat 4980
420 tgccaagcac gtccccatgc gctccatcaa gaagagcgac ttcgcggagc tggtgaagta 5040
422 catcaccgac gagcaaggca agaccgagcg cctttgcgac gctcaccggg ctggttgccc 5100
424 tcgccgctgg gctggcggcc gtctatggcc ctgcaaacgc gccagaaacg ccgtcgaagc 5160
426 cgtgtgcgag acaccgcggc cgccggcgtt gtggatacct cgcggaaaac ttggccctca 5220
428 ctgacagatg aggggcggac gttgacactt gaggggccga ctcacccggc gcggcgttga 5280
430 cagatgaggg gcaggctcga tttcggccgg cgacgtggag ctggccagcc tcgcaaatcg 5340
432 gcgaaaacgc ctgattttac gcgagtttcc cacagatgat gtggacaagc ctggggataa 5400
434 gtgccctgcg gtattgacac ttgaggggcg cgactactga cagatgaggg gcgcgatcct 5460
436 tgacacttga ggggcagagt gctgacagat gaggggcgca cctattgaca tttgaggggc 5520
438 tgtccacagg cagaaaatcc agcatttgca agggtttccg cccgttttc ggccaccgct 5580
440 aacctgtctt ttaacctgct tttaaaccaa tatttataaa ccttgttttt aaccagggct 5640
442 gcgccctgtg cgcgtgaccg cgcacgccga aggggggtgc ccccccttct cgaaccctcc 5700
444 cggcccgcta acgcgggcct cccatcccc cagggggctgc gccctcggc cgcgaacggc 5760
446 ctcaccccaa aaatggcagc gctggcagtc cttgccattg ccgggatcgg ggcagtaacg 5820
448 ggatgggcga tcagcccgag cgcgacgccc ggaagcattg acgtgccgca ggtgctggca 5880
450 tcgacattca gcgaccaggt gccgggcagt gagggcggcg gcctgggtgg cggcctgccc 5940
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454 ggcattcttg gcatagtggt cgcgggtgcc gtgctcgtgt cggggggtgc gataaaccca 6060
456 gcgaaccatt tgaggtgata ggtaagatta taccgaggta tgaaaacgag aattggacct 6120
458 ttacagaatt actctatgaa gcgccatatt taaaaagcta ccaagacgaa gaggatgaag 6180
460 aggatgagga ggcagattgc cttgaatata ttgacaatac tgataagata atatatcttt 6240
462 tatatagaag atatcgccgt atgtaaggat ttcaggggc aaggcatagg cagcgcgctt 6300
464 atcaatatat ctatagaatg ggcaaagcat aaaaacttgc atggactaat gcttgaaacc 6360
466 caggacaata accttatagc ttgtaaattc tatcataatt gggtaatgac tccaacttat 6420
```

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 07/05/2001
PATENT APPLICATION: **US/09/810,861A**   TIME: 10:31:40

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\07052001\I810861A.raw**

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:658 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   **SERIAL NUMBER:** 09/810,861A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
       Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
                        prevent "wrapping."

2_____Invalid Line Length   The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3_____Misaligned Amino   The numbering under each 5[th] amino acid is misaligned. Do **not** use tab codes between numbers;
     Numbering   use **space characters**, instead.

4_____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
                        ensure your subsequent submission is saved in ASCII text.**

5_____Variable Length   Sequence(s)_____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
                        each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
                        residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
     "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
                 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                 the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
                 Artificial or Unknown sequences.**

7_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
   (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                 (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                 This sequence is intentionally skipped

                 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8_____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
   (NEW RULES)   <210> sequence id number
                 <400> sequence id number
                 000

9_____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
   (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10___Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
     Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
                 is Artificial Sequence

11___Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                 "Unknown." Please explain source of genetic material in <220> to <223> section.
                 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12___PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
     "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.